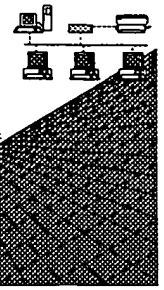


Shukla

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING **ERROR REPORT**

BEST AVAILABLE COPY

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/357,675
Art Unit / Team No. : 1632
Date Processed by STIC: 11/9/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/357,675

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)
- 12 _____ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Shukla

1632

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,675

DATE: 11/09/1999
TIME: 11:27:24

Input Set: I357675.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed
see p. 2, 100

1 <110> APPLICANT: Croce M.D., Carlo M.
2 <120> TITLE OF INVENTION: Nitrilase Homologs
3 <130> FILE REFERENCE: CRO01 NP001 Nitrilase Homologs
4 <140> CURRENT APPLICATION NUMBER: US/09/357,675
5 <141> CURRENT FILING DATE: 1999-07-20
6 <150> EARLIER APPLICATION NUMBER: 60/093,350
7 <151> EARLIER FILING DATE: 1998-07-20
8 <160> NUMBER OF SEQ ID NOS: 18
9 <170> SOFTWARE: PatentIn Ver. 2.1
10 <210> SEQ ID NO 1
11 <211> LENGTH: 1416
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapiens
14 <400> SEQUENCE: 1

see item 10 on Enr Summary Sheet

W-->

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17	tcaccaggcc	tcctcacaga	ttctgtccc	ttctgtgtcc	tggactccgg	atacctcaac	180
18	tctcagtact	ttgtgctcag	cccaggccca	gagccatggc	tatctcctct	tcctcctgcg	240
19	aactgcccc	ggtggctgtg	tgccaggtaa	catcgacgcc	agacaagcaa	cagaacttta	300
20	aaacatgtgc	tgagctgggt	cgagaggctg	ccagactggg	tgccctgctg	gctttcctgc	360
21	ctgaggcatt	tgacttcatt	gcacgggacc	ctgcagagac	gctacacctg	tctgaaccac	420
22	tggttgagg	acttttgaa	gaatacacc	agcttgccag	ggaatgtgga	ctctggctgt	480
23	ccttggtgg	tttccatgag	cgtggccaag	actgggagca	gactcagaaa	atctacaatt	540
24	gtcacgtgct	gctgaacagc	aaaggggcag	tagtgggccac	ttacaggaag	acacatctgt	600
25	gtgacgtaga	gattccagg	caggggccta	tgtgtgaaag	caactctacc	atgctggggc	660
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27	acatgcgggt	ccctgaactc	tctctggcat	tggctcaagc	tggagcagag	atacttacct	780
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32	gccgacacct	gcctgtgttc	cagcacccga	ggcctgacct	ctatggcaat	ctgggtcacc	1080
33	cactgtctta	agacttgact	tctgtgagtt	tagacctgcc	cctcccaccc	ccaccctgcc	1140
34	actatgagct	agtgtcatg	tgacttggag	gcaggatcca	ggcacagctc	ccctcacttg	1200
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36	gagcttcacc	tgaggtcaga	ctgcagtttc	agaaaggtgg	aattttatat	agtcattgtt	1320
37	tatttcattg	aaactgaagt	tctgctgagg	gctgagcagc	actggcattg	aaaaatataa	1380
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39 <210> SEQ ID NO 2
40 <211> LENGTH: 23
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
43 <400> SEQUENCE: 2
44 tctgaaactg cagtctgacc tca

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,675

DATE: 11/09/1999

TIME: 11:27:24

Input Set: I357675.RAW

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 47 <212> TYPE: DNA
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 49 <400> SEQUENCE: 3
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 65 <212> TYPE: DNA
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 71 <212> TYPE: DNA
 72 <213> ORGANISM: Drosophila melanogaster
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 75 <210> SEQ ID NO 8
 76 <211> LENGTH: 20
 77 <212> TYPE: DNA
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 93 <210> SEQ ID NO 11
 94 <211> LENGTH: 20

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/357,675DATE: 11/09/1999
TIME: 11:27:24

Input Set: I357675.RAW

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137	<212> TYPE: DNA	
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VERIFICATION SUMMARY
PATENT APPLICATION US/09/357,675DATE: 11/09/1999
TIME: 11:27:24

Input Set: I357675.RAW

Line	Error/Warning	Original Text
15	W "N" or "Xaa" used: Feature required	gcccactcgc tgcggcctnt ctggctccag accgcct
56	W "N" or "Xaa" used: Feature required	gtngtnccng gncaygtngt
62	W "N" or "Xaa" used: Feature required	acrtgnacrt gyttnacngt ytgngc